RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
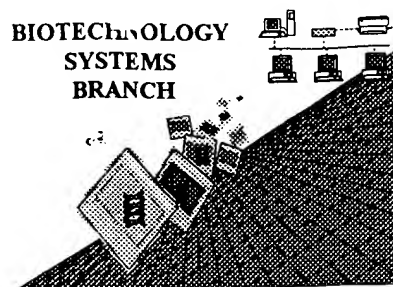BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/403,440_

Source: _1600 RUSH_

Date Processed by STIC: _7/10/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/403,440

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Davis.

1642

```
          RAW SEQUENCE LISTING              DATE: 07/10/2001
          PATENT APPLICATION:  US/09/403,440    TIME: 09:16:31

          Input Set : A:\09403440.txt
          Output Set: N:\CRF3\07102001\I403440.raw
```

Does Not Comply
Corrected Diskette Needed

pp 1-3

```
       1 <110> APPLICANT: Lane, David Philip
W-->   2 <120> TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO
W-->   3       INHIBITING THE INTERACTION OF p53 AND MDM2
W-->   4 <130> FILE REFERENCE: MEWB25.001APC
W-->   5 <140> CURRENT APPLICATION NUMBER: 09/403,440
C-->   6 <141> CURRENT FILING DATE: 2000-01-19
       7 <150> PRIOR APPLICATION NUMBER: PCT/GB98/01144
       8 <151> PRIOR FILING DATE: 1998-04-20
       9 <150> PRIOR APPLICATION NUMBER: GB 9708092.3
      10 <151> PRIOR FILING DATE: 1997-04-22
W-->  11 <160> NUMBER OF SEQ ID: 12
      12 <170> SOFTWARE: FastSEQ for Windows Version 4.0
      14 <210> SEQ ID NO: 1
      15 <211> LENGTH: 5
      16 <212> TYPE: PRT
      17 <213> ORGANISM: Unknown
W-->  18 <220> FEATURE:
      19 <223> OTHER INFORMATION: (Unknown)
      20 <221> NAME/KEY: UNSURE
      21 <222> LOCATION: 2,3
      22 <223> OTHER INFORMATION: Xaa = any amino acid
W-->  23 <400> SEQUENCE: 1
WOK   24       Phe Xaa Xaa Leu Trp
      25        1           5
      27 <210> SEQ ID NO: 2
      28 <211> LENGTH: 19
      29 <212> TYPE: PRT
      30 <213> ORGANISM: E. coli
W-->  31 <400> SEQUENCE: 2
      32       Pro Pro Leu Ser Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro
      33        1           5               10              15
      34       Glu Asn Gly
      36 <210> SEQ ID NO: 3
      37 <211> LENGTH: 19
      38 <212> TYPE: PRT
      39 <213> ORGANISM: E. coli
W-->  40 <400> SEQUENCE: 3
      41       Pro Pro Leu Ser Met Pro Arg Phe Met Asp Tyr Trp Glu Gly Leu Asn
      42        1           5               10              15
      43       Glu Asn Gly
      45 <210> SEQ ID NO: 4
      46 <211> LENGTH: 5
      47 <212> TYPE: PRT
      48 <213> ORGANISM: Unknown
W-->  49 <220> FEATURE:
      50 <223> OTHER INFORMATION: (Unknown)
      51 <221> NAME/KEY: UNSURE
```

give source of genetic material — see item 11 on Error Summary sheet

same error

```
      52 <222> LOCATION: 2,3,4
      53 <223> OTHER INFORMATION: Xaa= any amino acid
W--> 54 <400> SEQUENCE: 4
     55         Phe Xaa Xaa Xaa Trp
     56          1               5
     58 <210> SEQ ID NO: 5
     59 <211> LENGTH: 57
     60 <212> TYPE: DNA
     61 <213> ORGANISM: Artificial Sequence
W--> 62 <220> FEATURE:
     63 <223> OTHER INFORMATION: Synthetic peptide
W--> 64 <400> SEQUENCE: 5
     65         gtccgcctct gagtcaggaa acattttcag acctatggaa actacttcct gaaaacg     57
     67 <210> SEQ ID NO: 6
     68 <211> LENGTH: 57
     69 <212> TYPE: DNA
     70 <213> ORGANISM: Artificial Sequence
W--> 71 <220> FEATURE:
     72 <223> OTHER INFORMATION: Synthetic peptide
W--> 73 <400> SEQUENCE: 6
     74         gaccgttttc aggaagtagt ttccataggt ctgaaaatgt ttcctgactc agaggcg     57
     76 <210> SEQ ID NO: 7
     77 <211> LENGTH: 57
     78 <212> TYPE: DNA
     79 <213> ORGANISM: Artificial Sequence
W--> 80 <220> FEATURE:
     81 <223> OTHER INFORMATION: Synthetic peptide
W--> 82 <400> SEQUENCE: 7
     83         gtccgcctct gagtatgcct cgttttatgg attattggga gggtcttaat gaaaacg     57
     85 <210> SEQ ID NO: 8
     86 <211> LENGTH: 59
     87 <212> TYPE: DNA
     88 <213> ORGANISM: Artificial Sequence
W--> 89 <220> FEATURE:
     90 <223> OTHER INFORMATION: Synthetic peptide
W--> 91 <400> SEQUENCE: 8
     92         gaccgttttc attaagaccc tcccaataat ccataaaacg aggcatactc tcagaggcg     59
     94 <210> SEQ ID NO: 9
     95 <211> LENGTH: 35
     96 <212> TYPE: DNA
     97 <213> ORGANISM: Artificial Sequence
W--> 98 <220> FEATURE:
     99 <223> OTHER INFORMATION: OTHER INFORMATION: Synthetic peptide
W--> 100 <400> SEQUENCE: 9
    101         cgggatccac catgggcgat aaaattattc acctg
    103 <210> SEQ ID NO: 10
    104 <211> LENGTH: 29
    105 <212> TYPE: DNA
    106 <213> ORGANISM: Artificial Sequence
```

This is not a peptide sequence (handwritten annotation)

delete - do not use alphabetical headings (handwritten annotation)

not a peptide sequence (handwritten annotation)

35 (handwritten)

RAW SEQUENCE LISTING

DATE: 07/10/2001

PATENT APPLICATION: US/09/403,440

TIME: 09:16:31

Input Set : **A:\09403440.txt**
Output Set: **N:\CRF3\07102001\I403440.raw**

```
W--> 107 <220> FEATURE:
    108 <223> OTHER INFORMATION: Synthetic peptide
W--> 109 <400> SEQUENCE: 10
    110       ctcgacgcta acctggccta gggaattcc                        29
    112 <210> SEQ ID NO: 11
    113 <211> LENGTH: 26
    114 <212> TYPE: DNA
    115 <213> ORGANISM: Artificial Sequence
W--> 116 <220> FEATURE:
    117 <223> OTHER INFORMATION: Synthetic peptide
W--> 118 <400> SEQUENCE: 11
    119       gactctgggg atcgatatga ccgacc                          26
    121 <210> SEQ ID NO: 12
    122 <211> LENGTH: 27
    123 <212> TYPE: DNA
    124 <213> ORGANISM: Artificial Sequence
W--> 125 <220> FEATURE:
    126 <223> OTHER INFORMATION: Synthetic peptide
W--> 127 <400> SEQUENCE: 12
    128       gagccaggag acagcctcag gcttatg                         27
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/403,440**

DATE: 07/10/2001
TIME: 09:16:32

Input Set : **A:\09403440.txt**
Output Set: **N:\CRF3\07102001\I403440.raw**

```
L:2 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:283 W: Missing Blank Line separator, <140> field identifier
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:283 W: Missing Blank Line separator, <160> field identifier
L:18 M:283 W: Missing Blank Line separator, <220> field identifier
L:23 M:283 W: Missing Blank Line separator, <400> field identifier
L:24 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:31 M:283 W: Missing Blank Line separator, <400> field identifier
L:40 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:283 W: Missing Blank Line separator, <220> field identifier
L:54 M:283 W: Missing Blank Line separator, <400> field identifier
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:62 M:283 W: Missing Blank Line separator, <220> field identifier
L:64 M:283 W: Missing Blank Line separator, <400> field identifier
L:71 M:283 W: Missing Blank Line separator, <220> field identifier
L:73 M:283 W: Missing Blank Line separator, <400> field identifier
L:80 M:283 W: Missing Blank Line separator, <220> field identifier
L:82 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:283 W: Missing Blank Line separator, <220> field identifier
L:91 M:283 W: Missing Blank Line separator, <400> field identifier
L:98 M:283 W: Missing Blank Line separator, <220> field identifier
L:100 M:283 W: Missing Blank Line separator, <400> field identifier
L:107 M:283 W: Missing Blank Line separator, <220> field identifier
L:109 M:283 W: Missing Blank Line separator, <400> field identifier
L:116 M:283 W: Missing Blank Line separator, <220> field identifier
L:118 M:283 W: Missing Blank Line separator, <400> field identifier
L:125 M:283 W: Missing Blank Line separator, <220> field identifier
L:127 M:283 W: Missing Blank Line separator, <400> field identifier
```